IN THE CLAIMS:

1-9 (Cancelled).

10. (Currently Amended) A method for improving an electron density map of an experimental crystal structure, comprising the steps of:

~~a.~~(a) forming a model electron density map from known crystallographic information of [a] an exemplary model crystal structure;

~~b.~~(b) forming model histograms of model electron densities in identified protein and solvent regions of the model electron density map;

~~c.~~(c) fitting a model probability distribution function defined by

$$p(\rho_T) = \sum_k w_k \exp\left\{-\frac{(\rho - c_k)^2}{2\sigma_k^2}\right\}$$

to the model histograms, where k is separately indexed over the protein and solvent regions of the model map, $p(\rho_T)$ is a probability of an electron density at a point, w_k is a normalization factor, ρ is electron density, c_k is a mean value of ρ, and σ_k is a variance of ρ, where the fitting determines the coefficients w_k, c_k, and σ_k;

~~d.~~(d) determining a set of experimental structure factors from x-ray diffraction data for the experimental crystal structure and forming an experimental electron density map;

~~e.~~(e) forming separate experimental histograms of experimental electron densities over protein and solvent regions of the model electron density map;

~~f.~~(f) fitting an experimental probability distribution function defined by

~~$$p(\rho_T) = \sum_k w_k \exp\left\{\frac{(\rho - \beta c_k)^2}{2(\beta\sigma_k^2 + \sigma_{MAP}^2)}\right\}$$~~

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to separate protein and solvent regions of the experimental histograms, where β is an expectation that an experimental value of ρ is less than a true value and σ_{map} is a variance, where the fitting determines the coefficients β and σ_{map};

~~g.~~(g) determine ~~from the experimental probability distribution function~~ the overall experimental log-likelihood of the electron density in the protein and solvent regions of the experimental map from the experimental probability distribution function

$$LL\left(\rho\left(\mathbf{x},\{\mathbf{F}_h\}\right)\right)=\ln\left[p\left(\rho(\mathbf{x})|PROT\right)p_{PROT}(\mathbf{x})+p\left(\rho(\mathbf{x})|SOLV\right)p_{SOLV}(\mathbf{x})\right]$$

where $p_{PROT}(\mathbf{x})$ is the probability that $\mathbf{x}$ is in the protein region and $p\left(\rho(\mathbf{x})|PROT\right)$ is the conditional probability for $\rho(\mathbf{x})$ given that $\mathbf{x}$ is in the protein region, and $p_{SOLV}(\mathbf{x})$ and $p\left(\rho(\mathbf{x})|SOLV\right)$ are the corresponding quantities for the solvent region;

~~h.~~(h) determine how the experimental log-likelihood of the electron density of the protein and solvent regions of the structure factor experimental electron density map would change as each experimental changes to output a revised log-likelihood of any value of each experimental structure factor; [and]

~~i.~~(i) forming from the revised log-likelihood of experimental structure factor values a new set of structure factors ~~and returning the new set of structure factors to step (f) to iterate the process until changes to a new set of structure factors are below a predetermined value~~ ; and

(j) forming a revised experimental electron density map from the revised structure factors.

11. (Currently Amended) ~~A~~ The method according to Claim 10, wherein step ~~a.~~ (a) further includes a step of selecting the model crystal structure to be similar in size, data resolution, and atomic displacement factors to the experimental crystal structure.

12. (Currently Amended) ~~A~~ The method according to Claim 10, wherein step ~~b.~~ (b) further includes a step of identifying protein and solvent regions by designating all points within a selected distance of an atom as "protein" and all other points ~~at~~ as "solvent."

13. (Currently Amended) ~~A~~ The method according to Claim 11, wherein step ~~b.~~ (b) further includes a step of identifying protein and solvent regions by designating all

points within a selected distance of an atom as "protein" and all other points ~~at~~ as "solvent."

14. (Currently Amended) ~~A~~ The method according to Claim 10, wherein step ~~h.~~ (h) includes steps of forming a Taylor's series expansion of the log-likelihood of the experimental electron density map and evaluating terms of the Taylor's series expansion using a Fast Fourier Transform.